

1635 1600

CRF Errors Corrected by the STIC Systems Branch

Serial Number: 09/700,906B

CRF Processing Date: 11/21/2002
Edited by: A (STIC staff)
Verified by:**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line. #15
- ☐ Edited a format error in the Current Application Data section, specifically:
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

RECEIVED
DEC 04 2002
TECH CENTER 1600/2900

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



1600

RAW SEQUENCE LISTING

DATE: 11/21/2002

PATENT APPLICATION: US/09/700,906B

TIME: 10:13:50

Input Set : A:\US Serial 09-700906-Sequence-List-11-06-02.txt

Output Set: N:\CRF4\11212002\I700906B.raw

4 <110> APPLICANT: Faustus Forschungs Cie. Translational Cancer Research GmbH
 6 <120> TITLE OF INVENTION: Antisense oligonucleotides for treating proliferating cells
 8 <130> FILE REFERENCE: PA32470US-01938
 10 <140> CURRENT APPLICATION NUMBER: US/09/700,906B
 11 <141> CURRENT FILING DATE: 2001-02-26
 13 <150> PRIOR APPLICATION NUMBER: DE 198 22 954.2
 14 <151> PRIOR FILING DATE: 1998-05-22
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn Vers. 2.0

ERRORED SEQUENCES

1582 <210> SEQ ID NO: 5
 1583 <211> LENGTH: 25
 1584 <212> TYPE: DNA
 1585 <213> ORGANISM: Artificial sequence
 1587 <220> FEATURE:
 1588 <223> OTHER INFORMATION: Description of the artificial sequence: missense
 1589 Synthetic oligonucleotide
 1591 <400> SEQUENCE: 5
 1592 agtactcagt aacgcctacg gtaag

25

E--> 1594 ~~-42-~~*delete*

Does Not Comply
Corrected Diskette Needed

ef

VERIFICATION SUMMARY

DATE: 11/21/2002

PATENT APPLICATION: **US/09/700,906B**

TIME: 10:13:51

Input Set : **A:\US Serial 09-700906-Sequence-List-11-06-02.txt**

Output Set: **N:\CRF4\11212002\I700906B.raw**

L:1594 M:254 E: No. of Bases conflict, this line has no nucleotides.



1600

RAW SEQUENCE LISTING

DATE: 11/27/2002

PATENT APPLICATION: US/09/700,906B

TIME: 18:13:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11272002\I700906B.raw

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4 <110> APPLICANT: Faustus Forschungs Cie. Translational Cancer Research GmbH
6 <120> TITLE OF INVENTION: Antisense oligonucleotides for treating proliferating cells
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13 <150> PRIOR APPLICATION NUMBER: DE 198 22 954.2
14 <151> PRIOR FILING DATE: 1998-05-22
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn Vers. 2.0
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21 <211> LENGTH: 12493
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (197)..(9964)
29 <400> SEQUENCE: 1
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32 gacgagcggt gggtcgacaa gtggccttgc gggccggatc gtcccagtg aagagttgta 120
34 aatttgcttc tggccttccc ctacggatta tacctggcct tcccctacgg attatactca 180
36 acttactgtt tagaaa atg tgg ccc acg aga cgc ctg gtt act atc aaa agg 232
37          Met Trp Pro Thr Arg Arg Leu Val Thr Ile Lys Arg
38          1          5          10
40 agc ggg gtc gac ggt ccc cac ttt ccc ctg agc ctc agc acc tgc ttg 280
41 Ser Gly Val Asp Gly Pro His Phe Pro Leu Ser Leu Ser Thr Cys Leu
42          15          20          25
44 ttt gga agg ggt att gaa tgt gac atc cgt atc cag ctt cct gtt gtg 328
45 Phe Gly Arg Gly Ile Glu Cys Asp Ile Arg Ile Gln Leu Pro Val Val
46          30          35          40
48 tca aaa caa cat tgc aaa gtt gaa atc cat gag cag gag gca ata tta 376
49 Ser Lys Gln His Cys Lys Val Glu Ile His Glu Gln Glu Ala Ile Leu
50 45          50          55          60
52 cat aat ttc agt tcc aca aat cca aca caa gta aat ggg tct gtt att 424
53 His Asn Phe Ser Ser Thr Asn Pro Thr Gln Val Asn Gly Ser Val Ile
54          65          70          75
56 gat gag cct gta cgg cta aaa cat gga gat gta ata act att att gat 472
57 Asp Glu Pro Val Arg Leu Lys His Gly Asp Val Ile Thr Ile Ile Asp
58          80          85          90
60 cgt tcc ttc agg tat gaa aat gaa agt ctt cag aat gga agg aag tca 520
61 Arg Ser Phe Arg Tyr Glu Asn Glu Ser Leu Gln Asn Gly Arg Lys Ser
62          95          100          105
64 act gaa ttt cca aga aaa ata cgt gaa cag gag cca gca cgt cgt gtc 568
65 Thr Glu Phe Pro Arg Lys Ile Arg Glu Gln Glu Pro Ala Arg Arg Val

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TIME: 18:13:46

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\11272002\I700906B.raw

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69 Ser Arg Ser Ser Phe Ser Ser Asp Pro Asp Glu Lys Ala Gln Asp Ser
70 125      130      135      140
72 aag gcc tat tca aaa atc act gaa gga aaa gtt tca gga aat cct cag 664
73 Lys Ala Tyr Ser Lys Ile Thr Glu Gly Lys Val Ser Gly Asn Pro Gln
74      145      150      155
76 gta cat atc aag aat gtc aaa gaa gac agt acc gca gat gac tca aaa 712
77 Val His Ile Lys Asn Val Lys Glu Asp Ser Thr Ala Asp Asp Ser Lys
78      160      165      170
80 gac agt gtt gct cag gga aca act aat gtt cat tcc tca gaa cat gct 760
81 Asp Ser Val Ala Gln Gly Thr Thr Asn Val His Ser Ser Glu His Ala
82      175      180      185
84 gga cgt aat ggc aga aat gca gct gat ccc att tct ggg gat ttt aaa 808
85 Gly Arg Asn Gly Arg Asn Ala Ala Asp Pro Ile Ser Gly Asp Phe Lys
86      190      195      200
88 gaa att tcc agc gtt aaa tta gtg agc cgt tat gga gaa ttg aag tct 856
89 Glu Ile Ser Ser Val Lys Leu Val Ser Arg Tyr Gly Glu Leu Lys Ser
90 205      210      215      220
92 gtt ccc act aca caa tgt ctt gac aat agc aaa aaa aat gaa tct ccc 904
93 Val Pro Thr Thr Gln Cys Leu Asp Asn Ser Lys Lys Asn Glu Ser Pro
94      225      230      235
96 ttt tgg aag ctt tat gag tca gtg aag aaa gag ttg gat gta aaa tca 952
97 Phe Trp Lys Leu Tyr Glu Ser Val Lys Lys Glu Leu Asp Val Lys Ser
98      240      245      250
100 caa aaa gaa aat gtc cta cag tat tgt aga aaa tct gga tta caa act 1000
101 Gln Lys Glu Asn Val Leu Gln Tyr Cys Arg Lys Ser Gly Leu Gln Thr
102      255      260      265
104 gat tac gca aca gag aaa gaa agt gct gat ggt tta cag ggg gag acc 1048
105 Asp Tyr Ala Thr Glu Lys Glu Ser Ala Asp Gly Leu Gln Gly Glu Thr
106      270      275      280
108 caa ctg ttg gtc tcg cgt aag tca aga cca aaa tct ggt ggg agc ggc 1096
109 Gln Leu Leu Val Ser Arg Lys Ser Arg Pro Lys Ser Gly Gly Ser Gly
110 285      290      295      300
112 cac gct gtg gca gag cct gct tca cct gaa caa gag ctt gac cag aac 1144
113 His Ala Val Ala Glu Pro Ala Ser Pro Glu Gln Glu Leu Asp Gln Asn
114      305      310      315
116 aag ggg aag gga aga gac gtg gag tct gtt cag act ccc agc aag gct 1192
117 Lys Gly Lys Gly Arg Asp Val Glu Ser Val Gln Thr Pro Ser Lys Ala
118      320      325      330
120 gtg ggc gcc agc ttt cct ctc tat gag ccg gct aaa atg aag acc cct 1240
121 Val Gly Ala Ser Phe Pro Leu Tyr Glu Pro Ala Lys Met Lys Thr Pro
122      335      340      345
124 gta caa tat tca cag caa caa aat tct cca caa aaa cat aag aac aaa 1288
125 Val Gln Tyr Ser Gln Gln Asn Ser Pro Gln Lys His Lys Asn Lys
126      350      355      360
128 gac ctg tat act act ggt aga aga gaa tct gtg aat ctg ggt aaa agt 1336
129 Asp Leu Tyr Thr Thr Gly Arg Arg Glu Ser Val Asn Leu Gly Lys Ser
130 365      370      375      380

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TIME: 18:13:46

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132	gaa ggc ttc aag gct ggt gat aaa act ctt act ccc agg aag ctt tca	1384
133	Glu Gly Phe Lys Ala Gly Asp Lys Thr Leu Thr Pro Arg Lys Leu Ser	
134	385 390 395	
136	act aga aat cga aca cca gct aaa gtt gaa gat gca gct gac tct gcc	1432
137	Thr Arg Asn Arg Thr Pro Ala Lys Val Glu Asp Ala Ala Asp Ser Ala	
138	400 405 410	
140	act aag cca gaa aat ctc tct tcc aaa acc aga gga agt att cct aca	1480
141	Thr Lys Pro Glu Asn Leu Ser Ser Lys Thr Arg Gly Ser Ile Pro Thr	
142	415 420 425	
144	gat gtg gaa gtt ctg cct acg gaa act gaa att cac aat gag cca ttt	1528
145	Asp Val Glu Val Leu Pro Thr Glu Thr Glu Ile His Asn Glu Pro Phe	
146	430 435 440	
148	tta act ctg tgg ctc act caa gtt gag agg aag atc caa aag gat tcc	1576
149	Leu Thr Leu Trp Leu Thr Gln Val Glu Arg Lys Ile Gln Lys Asp Ser	
150	445 450 455 460	
152	ctc agc aag cct gag aaa ttg ggc act aca gct gga cag atg tgc tct	1624
153	Leu Ser Lys Pro Glu Lys Leu Gly Thr Thr Ala Gly Gln Met Cys Ser	
154	465 470 475	
156	ggg tta cct ggt ctt agt tca gtt gat atc aac aac ttt ggt gat tcc	1672
157	Gly Leu Pro Gly Leu Ser Ser Val Asp Ile Asn Asn Phe Gly Asp Ser	
158	480 485 490	
160	att aat gag agt gag gga ata cct ttg aaa aga agg cgt gtg tcc ttt	1720
161	Ile Asn Glu Ser Glu Gly Ile Pro Leu Lys Arg Arg Arg Val Ser Phe	
162	495 500 505	
164	ggt ggg cac cta aga cct gaa cta ttt gat gaa aac ttg cct cct aat	1768
165	Gly Gly His Leu Arg Pro Glu Leu Phe Asp Glu Asn Leu Pro Pro Asn	
166	510 515 520	
168	acg cct ctc aaa agg gga gaa gcc cca acc aaa aga aag tct ctg gta	1816
169	Thr Pro Leu Lys Arg Gly Glu Ala Pro Thr Lys Arg Lys Ser Leu Val	
170	525 530 535 540	
172	atg cac act cca cct gtc ctg aag aaa atc atc aag gaa cag cct caa	1864
173	Met His Thr Pro Pro Val Leu Lys Lys Ile Ile Lys Glu Gln Pro Gln	
174	545 550 555	
176	cca tca gga aaa caa gag tca ggt tca gaa atc cat gtg gaa gtg aag	1912
177	Pro Ser Gly Lys Gln Glu Ser Gly Ser Glu Ile His Val Glu Val Lys	
178	560 565 570	
180	gca caa agc ttg gtt ata agc cct cca gct cct agt cct agg aaa act	1960
181	Ala Gln Ser Leu Val Ile Ser Pro Pro Ala Pro Ser Pro Arg Lys Thr	
182	575 580 585	
184	cca gtt gcc agt gat caa cgc cgt agg tcc tgc aaa aca gcc cct gct	2008
185	Pro Val Ala Ser Asp Gln Arg Arg Arg Ser Cys Lys Thr Ala Pro Ala	
186	590 595 600	
188	tcc agc agc aaa tct cag aca gag gtt cct aag aga gga gga gaa aga	2056
189	Ser Ser Ser Lys Ser Gln Thr Glu Val Pro Lys Arg Gly Gly Glu Arg	
190	605 610 615 620	
192	gtg gca acc tgc ctt caa aag aga gtg tct atc agc cga agt caa cat	2104
193	Val Ala Thr Cys Leu Gln Lys Arg Val Ser Ile Ser Arg Ser Gln His	
194	625 630 635	
196	gat att tta cag atg ata tgt tcc aaa aga aga agt ggt gct tcg gaa	2152

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Output Set: N:\CRF4\11272002\I700906B.raw

197	Asp	Ile	Leu	Gln	Met	Ile	Cys	Ser	Lys	Arg	Arg	Ser	Gly	Ala	Ser	Glu	
198				640					645					650			
200	gca	aat	ctg	att	gtt	gca	aaa	tca	tgg	gca	gat	gta	gta	aaa	ctt	ggt	2200
201	Ala	Asn	Leu	Ile	Val	Ala	Lys	Ser	Trp	Ala	Asp	Val	Val	Lys	Leu	Gly	
202				655					660					665			
204	gca	aaa	caa	aca	caa	act	aaa	gtc	ata	aaa	cat	ggt	cct	caa	agg	tca	2248
205	Ala	Lys	Gln	Thr	Gln	Thr	Lys	Val	Ile	Lys	His	Gly	Pro	Gln	Arg	Ser	
206				670					675					680			
208	atg	aac	aaa	agg	caa	aga	aga	cct	gct	act	cca	aag	aag	cct	gtg	ggc	2296
209	Met	Asn	Lys	Arg	Gln	Arg	Arg	Pro	Ala	Thr	Pro	Lys	Lys	Pro	Val	Gly	
210	685						690					695				700	
212	gaa	gtt	cac	agt	caa	ttt	agt	aca	ggc	cac	gca	aac	tct	cct	tgt	acc	2344
213	Glu	Val	His	Ser	Gln	Phe	Ser	Thr	Gly	His	Ala	Asn	Ser	Pro	Cys	Thr	
214					705					710					715		
216	ata	ata	ata	ggg	aaa	gct	cat	act	gaa	aaa	gta	cat	gtg	cct	gct	cga	2392
217	Ile	Ile	Ile	Gly	Lys	Ala	His	Thr	Glu	Lys	Val	His	Val	Pro	Ala	Arg	
218				720						725					730		
220	ccc	tac	aga	gtg	ctc	aac	aac	ttc	att	tcc	aac	caa	aaa	atg	gac	ttt	2440
221	Pro	Tyr	Arg	Val	Leu	Asn	Asn	Phe	Ile	Ser	Asn	Gln	Lys	Met	Asp	Phe	
222				735						740				745			
224	aag	gaa	gat	ctt	tca	gga	ata	gct	gaa	atg	ttc	aag	acc	cca	gtg	aag	2488
225	Lys	Glu	Asp	Leu	Ser	Gly	Ile	Ala	Glu	Met	Phe	Lys	Thr	Pro	Val	Lys	
226				750						755				760			
228	gag	caa	ccg	cag	ttg	aca	agc	aca	tgt	cac	atc	gct	att	tca	aat	tca	2536
229	Glu	Gln	Pro	Gln	Leu	Thr	Ser	Thr	Cys	His	Ile	Ala	Ile	Ser	Asn	Ser	
230	765					770					775					780	
232	gag	aat	ttg	ctt	gga	aaa	cag	ttt	caa	gga	act	gat	tca	gga	gaa	gaa	2584
233	Glu	Asn	Leu	Leu	Gly	Lys	Gln	Phe	Gln	Gly	Thr	Asp	Ser	Gly	Glu	Glu	
234					785					790					795		
236	cct	ctg	ctc	ccc	acc	tca	gag	agt	ttt	gga	gga	aat	gtg	ttc	ttc	agt	2632
237	Pro	Leu	Leu	Pro	Thr	Ser	Glu	Ser	Phe	Gly	Gly	Asn	Val	Phe	Phe	Ser	
238				800						805					810		
240	gca	cag	aat	gca	gca	aaa	cag	cca	tct	gat	aaa	tgc	tct	gca	agc	cct	2680
241	Ala	Gln	Asn	Ala	Ala	Lys	Gln	Pro	Ser	Asp	Lys	Cys	Ser	Ala	Ser	Pro	
242				815						820				825			
244	ccc	tta	aga	cgg	cag	tgt	att	aga	gaa	aat	gga	aac	gta	gca	aaa	acg	2728
245	Pro	Leu	Arg	Arg	Gln	Cys	Ile	Arg	Glu	Asn	Gly	Asn	Val	Ala	Lys	Thr	
246				830						835				840			
248	ccc	agg	aac	acc	tac	aaa	atg	act	tct	ctg	gag	aca	aaa	act	tca	gat	2776
249	Pro	Arg	Asn	Thr	Tyr	Lys	Met	Thr	Ser	Leu	Glu	Thr	Lys	Thr	Ser	Asp	
250	845					850					855					860	
252	act	gag	aca	gag	cct	tca	aaa	aca	gta	tcc	act	gta	aac	agg	tca	gga	2824
253	Thr	Glu	Thr	Glu	Pro	Ser	Lys	Thr	Val	Ser	Thr	Val	Asn	Arg	Ser	Gly	
254					865					870					875		
256	agg	tct	aca	gag	ttc	agg	aat	ata	cag	aag	cta	cct	gtg	gaa	agt	aag	2872
257	Arg	Ser	Thr	Glu	Phe	Arg	Asn	Ile	Gln	Lys	Leu	Pro	Val	Glu	Ser	Lys	
258					880					885					890		
260	agt	gaa	gaa	aca	aat	aca	gaa	att	gtt	gag	tgc	atc	cta	aaa	aga	ggt	2920
261	Ser	Glu	Glu	Thr	Asn	Thr	Glu	Ile	Val	Glu	Cys	Ile	Leu	Lys	Arg	Gly	

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Input Set : A:\PTO.AMC.txt

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265	Gln Lys Ala Thr Leu Leu Gln Gln Arg Arg Glu Gly Glu Met Lys Glu			
266	910	915	920	
268	ata gaa aga cct ttt gag aca tat aag gaa aat att gaa tta aaa gaa	3016		
269	Ile Glu Arg Pro Phe Glu Thr Tyr Lys Glu Asn Ile Glu Leu Lys Glu			
270	925	930	935	940
272	aac gat gaa aag atg aaa gca atg aag aga tca aga act tgg ggg cag	3064		
273	Asn Asp Glu Lys Met Lys Ala Met Lys Arg Ser Arg Thr Trp Gly Gln			
274	945	950	955	
276	aaa tgt gca cca atg tct gac ctg aca gac ctc aag agc ttg cct gat	3112		
277	Lys Cys Ala Pro Met Ser Asp Leu Thr Asp Leu Lys Ser Leu Pro Asp			
278	960	965	970	
280	aca gaa ctc atg aaa gac acg gca cgt ggc cag aat ctc ctc caa acc	3160		
281	Thr Glu Leu Met Lys Asp Thr Ala Arg Gly Gln Asn Leu Leu Gln Thr			
282	975	980	985	
284	caa gat cat gcc aag gca cca aag agt gag aaa ggc aaa atc act aaa	3208		
285	Gln Asp His Ala Lys Ala Pro Lys Ser Glu Lys Gly Lys Ile Thr Lys			
286	990	995	1000	
288	atg ccc tgc cag tca tta caa cca gaa cca ata aac acc cca aca cac	3256		
289	Met Pro Cys Gln Ser Leu Gln Pro Glu Pro Ile Asn Thr Pro Thr His			
290	1005	1010	1015	1020
292	aca aaa caa cag ttg aag gca tcc ctg ggg aaa gta ggt gtg aaa gaa	3304		
293	Thr Lys Gln Gln Leu Lys Ala Ser Leu Gly Lys Val Gly Val Lys Glu			
294	1025	1030	1035	
296	gag ctc cta gca gtc ggc aag ttc aca cgg acg tca ggg gag acc acg	3352		
297	Glu Leu Leu Ala Val Gly Lys Phe Thr Arg Thr Ser Gly Glu Thr Thr			
298	1040	1045	1050	
300	cac acg cac aga gag cca gca gga gat ggc aag agc atc aga acg ttt	3400		
301	His Thr His Arg Glu Pro Ala Gly Asp Gly Lys Ser Ile Arg Thr Phe			
302	1055	1060	1065	
304	aag gag tct cca aag cag atc ctg gac cca gca gcc cgt gta act gga	3448		
305	Lys Glu Ser Pro Lys Gln Ile Leu Asp Pro Ala Ala Arg Val Thr Gly			
306	1070	1075	1080	
308	atg aag aag tgg cca aga acg cct aag gaa gag gcc cag tca cta gaa	3496		
309	Met Lys Lys Trp Pro Arg Thr Pro Lys Glu Glu Ala Gln Ser Leu Glu			
310	1085	1090	1095	1100
312	gac ctg gct ggc ttc aaa gag ctc ttc cag aca cca ggt ccc tct gag	3544		
313	Asp Leu Ala Gly Phe Lys Glu Leu Phe Gln Thr Pro Gly Pro Ser Glu			
314	1105	1110	1115	
316	gaa tca atg act gat gag aaa act acc aaa ata gcc tgc aaa tct cca	3592		
317	Glu Ser Met Thr Asp Glu Lys Thr Thr Lys Ile Ala Cys Lys Ser Pro			
318	1120	1125	1130	
320	cca cca gaa tca gtg gac act cca aca agc aca aag caa tgg cct aag	3640		
321	Pro Pro Glu Ser Val Asp Thr Pro Thr Ser Thr Lys Gln Trp Pro Lys			
322	1135	1140	1145	
324	aga agt ctc agg aaa gca gat gta gag gaa gaa ttc tta gca ctc agg	3688		
325	Arg Ser Leu Arg Lys Ala Asp Val Glu Glu Glu Phe Leu Ala Leu Arg			
326	1150	1155	1160	

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